```
    130                 135                 140

Thr Phe Gly Ser Arg Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr
145                 150                 155                 160

Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys
                165                 170                 175

Gly Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
            180                 185                 190

Ala Leu Gln Asn Ala Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg
        195                 200                 205

Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu
    210                 215                 220

Val His Phe Met Lys Arg Leu Pro Arg Gly His His Thr Thr Glu Gln
225                 230                 235                 240

Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu
                245                 250                 255

Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg
            260                 265
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<210> 23
<211> 4177
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (593)..(1216)

<400> 23
ggaattccgg gaagagaggg aagaaaacaa cggcgactgg gcagctgcct ccacttctga 60

caactccaaa gggatatact tgtagaagtg gctcgcaggc tggggctccg cagagagaga 120

ccagaaggtg ccaaccgcag aggggtgcag atatctcccc ctattcccca ccccacctcc 180

cttgggtttt gttcaccgtg ctgtcatctg tttttcagac ctttttggca tctaacatgg 240

tgaagaaagg agtaaagaag agaacaaagt aactcctggg ggagcgaaga gcgctggtga 300

ccaacaccac caacgccacc accagctcct gctgctgcgg ccacccacgt ccaccattta 360

ccgggaggct ccagaggcgt aggcagcgga tccgagaaag gagcgagggg agtcagccgg 420

cttttccgag gagttatgga tgttggtgca ttcacttctg gccagatccg cgcccagagg 480

gagctaacca gcagccacca cctcgagctc tctccttgcc ttgcatcggg tcttaccctt 540

ccagtatgtt ccttctgatg agacaatttc cagtgccgag agtttcagta ca atg tgg 598
                                                        Met Trp
                                                          1

aaa tgg ata ctg aca cat tgt gcc tca gcc ttt ccc cac ctg ccc ggc 646
Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly
  5   10   15

```
tgc tgc tgc tgc tgc ttt ttg ttg ctg ttc ttg gtg tct tcc gtc cct   694
Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro
     20                  25                  30

gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag gcc acc   742
Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 35                  40                  45                  50

aac tct tct tcc tcc tcc ttc tcc tct cct tcc agc gcg gga agg cat   790
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
                 55                  60                  65

gtg cgg agc tac aat cac ctt caa gga gat gtc cgc tgg aga aag cta   838
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
             70                  75                  80

ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg aag gtc   886
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
         85                  90                  95

agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca   934
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
    100                 105                 110

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat   982
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
115                 120                 125                 130

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt  1030
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
                135                 140                 145

aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat  1078
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
            150                 155                 160

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg  1126
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
        165                 170                 175

gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg  1174
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
    180                 185                 190

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca          1216
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195                 200                 205

tagaggaagg caacgtttgt ggatgcagta aaaccaatgg ctcttttgcc aagaatagtg 1276

gatattcttc atgaagacag tagattgaaa ggcaaagaca cgttgcagat gtctgcttgc 1336

ttaaaagaaa gccagccttt gaaggttttt gtattcactg ctgacatatg atgttctttt 1396

aattagttct gtgtcatgtc ttataatcaa gatataggca gatcgaatgg gatagaagtt 1456

attcccaagt gaaaaacatt gtggctgggt tttttgttgt tgttgtcaag tttttgtttt 1516

taaacctctg agatagaact taaaggacat agaacaatct gttgaaagaa cgatcttcgg 1576

gaaagttatt tatggaatac gaactcatat caaagacttc attgctcatt caagcctaat 1636
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gaatcaatga acagtaatac gtgcaagcat ttactggaaa gcacttgggt catatcatat 1696

gcacaaccaa aggagttctg gatgtggtct catggaataa ttgaatagaa tttaaaaata 1756

taaacatgtt agtgtgaaac tgttctaaca atacaaatag tatggtatgc ttgtgcattc 1816

tgccttcatc cctttctatt tctttctaag ttatttattt aataggatgt taaatatctt 1876

ttggggtttt aaagagtatc tcagcagctg tcttctgatt tatcttttct ttttattcag 1936

cacaccacat gcatgttcac gacaaagtgt ttttaaaact tggcgaacac ttcaaaaata 1996

ggagttggga ttagggaagc agtatgagtg cccgtgtgct atcagttgac ttaatttgca 2056

cttctgcagt aataaccatc aacaataaat atggcaatgc tgtgccatgg cttgagtgag 2116

agatgtctgc tatcatttga aaacatatat tactctcgag gcttcctgtc tcaagaaata 2176

gaccagaagg ccaaattctt ctctttcaat acatcagttt gcctccaaga atatactaaa 2236

aaaaggaaaa ttaattgcta aatacattta aatagcctag cctcattatt tactcatgat 2296

ttcttgccaa atgtcatggc ggtaaagagg ctgtccacat ctctaaaaac cctctgtaaa 2356

ttccacataa tgcatctttc ccaaaggaac tataaagaat ttggtatgaa gcgcaactct 2416

cccaggggct taaactgagc aaatcaaata tatactggta tatgtgtaac catatacaaa 2476

aacctgttct agctgtatga tctagtcttt acaaaaccaa ataaaacttg ttttctgtaa 2536

atttaaagag ctttacaagg ttccataatg taaccatatc aaaattcatt ttgttagagc 2596

acgtatagaa aagagtacat aagagtttac caatcatcat cacattgtat tccactaaat 2656

aaatacataa gccttatttg cagtgtctgt agtgatttta aaaatgtaga aaaatactat 2716

ttgttctaaa tacttttaag caataactat aatagtatat tgatgctgca gttttatctt 2776

catatttctt gttttgaaaa agcattttat tgtttggaca cagtattttg gtacaaaaaa 2836

aaagactcac taaatgtgtc ttactaaagt ttaacctttg gaaatgctgg cgttctgtga 2896

ttctccaaca aacttatttg tgtcaatact taaccagcac ttccagttaa tctgttattt 2956

ttaaaaattg ctttattaag aaatttttg tataatccca taaaaggtca tatttttccc 3016

attcttcaaa aaaactgtat ttcagaagaa acacatttga ggcactgtct tttggcttat 3076

agtttaaatt gcatttcatc atactttgct tccaacttgc tttttggcaa atgagattat 3136

aaaaatgttt aatttttgtg gttggaatct ggatgttaaa atttaattgg taactcagtc 3196

tgtgagctat aatgtaatgc attcctatcc aaactaggta tctttttttc ctttatgttg 3256

aaataataat ggcacctgac acatagacat agaccaccca caacctaaat taaatgtttg 3316

gtaagacaaa tacacattgg atgaccacag taacagcaaa cagggcacaa actggattct 3376

tatttcacat agacatttag attactaaag agggctatgt gtaaacagtc atcattatag 3436

tactcaagac actaaaacag cttctagcca aatatattaa agcttgcaga ggccaaaaat 3496

agaaaacatc tcccctgtct ctcccacatt tccctcacag aaagacaaaa aacctgcctg 3556

gtgcagtagc tcacacctgt aatcccagca gtttgggaga ctgtgggaag atggcttgag 3616

tccaggagtt ctagacaggc ctgagaaacc tagtgagaca tccttctctt aaacaaaaca 3676

aaacaaaaca aatgtagcca tgcgtggtgg catatacctg tggtcccaac tactcaggag 3736

gctgaaacgg aaggatctct tgggccccag gagtttgagg ctgcagtgag ctataatctt 3796

gccattgcac tccagcctgg gtgaaaaaga gccagaaaga aaggaaagag agaaaagaga 3856

aaagaaagag agaaaagaca gaaagacagg aaggaaggaa ggaaggaagg aaggaaggaa 3916

ggaagcaagg aaagaaggaa ggaaggaaag aagggaggga aggaaggaga gagaaagaaa 3976

gattgtttgg taaggagtaa tgacattctc ttgcatttaa aagtggcata tttgcttgaa 4036

atggaaatag aattctggtc ccttttgcaa ctactgaaga aaaaaaaaag cagtttcagc 4096

cctgaatgtt gtagatttga aaaaaaaaaa aaaaaaactc gaggggggge ccgtacccaa 4156

ttcgccctat agtgagtcgt a 4177

<210> 24
<211> 208
<212> PRT
<213> Homo sapiens

<400> 24
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15

Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45

Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
50 55 60

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
115 120 125

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
130 135 140

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145 150 155 160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met

165 170 175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

<210> 25
<211> 31
<212> PRT
<213> Homo sapiens

<400> 25
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
1 5 10 15

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn
20 25 30

<210> 26
<211> 19
<212> PRT
<213> Homo sapiens

<400> 26
Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys
1 5 10 15

Pro Tyr Ser

<210> 27
<211> 30
<212> PRT
<213> Homo sapiens

<400> 27
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
1 5 10 15

Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
20 25 30

<210> 28
<211> 19
<212> PRT
<213> Homo sapiens

<400> 28
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn
1 5 10 15

Thr Ser Ala

<210> 29
<211> 555
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(552)

<220>
<223> Description of Artificial Sequence: pQE60-Cys37 construct

<400> 29

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atg aga gga tcg cat cac cat cac cat cac gga tcc tgc cag gct ctg   48
Met Arg Gly Ser His His His His His His Gly Ser Cys Gln Ala Leu
  1               5                  10                  15

ggt cag gac atg gtt tct ccg gaa gct acc aac tct tcc tct tcc tct   96
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
             20                  25                  30

ttc tct tcc ccg tct tcc gct ggt cgt cac gtt cgt tct tac aac cac   144
Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His
         35                  40                  45

ctg cag ggt gac gtt cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac   192
Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr
     50                  55                  60

ttc ctg aaa atc gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag   240
Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu
 65                  70                  75                  80

aac tgc ccg tac agc atc ctg gag ata aca tca gta gaa atc gga gtt   288
Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
                 85                  90                  95

gtt gcc gtc aaa gcc att aac agc aac tat tac tta gcc atg aac aag   336
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys
            100                 105                 110

aag ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg   384
Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
        115                 120                 125

aag gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac   432
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
    130                 135                 140

tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga   480
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
145                 150                 155                 160

gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac   528
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
                165                 170                 175

ttt ctt cca atg gtg gta cac tca tag                              555
Phe Leu Pro Met Val Val His Ser
            180
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<210> 30
<211> 184
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pQE60-Cys37
construct

<400> 30
Met Arg Gly Ser His His His His His His Gly Ser Cys Gln Ala Leu
1 5 10 15

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
20 25 30

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His
35 40 45

Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr
50 55 60

Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu
65 70 75 80

Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
85 90 95

Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys
100 105 110

Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
115 120 125

Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
130 135 140

Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
145 150 155 160

Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
165 170 175

Phe Leu Pro Met Val Val His Ser
180

<210> 31
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 31
atgtggaaat ggatactgac ccactgcgct tctgctttcc cgcacctgcc gggttgctgc 60
tgctgctgct tcctgctgct gttc 84

<210> 32
<211> 82

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 32
ccggagaaac catgtcctga cccagagcct ggcaggtaac cggaacagaa gaaaccagga 60
acagcagcag gaagcagcag ca 82

<210> 33
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 33
gggtcaggac atggtttctc cggaagctac caactcttct tcttcttctt tctcttctcc 60
gtcttctgct ggtcgtcacg 80

<210> 34
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 34
ggtgaaagag aacagtttac gccaacgaac gtcaccctgc aggtggttgt aagaacgaac 60
gtgacgacca gcagaagacg g 81

<210> 35
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 35
cgttggcgta aactgttctc tttcaccaaa tacttcctga aaatcgaaaa aaacggtaaa 60
gtttctggga ccaaa 75

<210> 36
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 36
tttggtccca gaaactttac cgtttttttc gattttcag 39

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 37
aaaggatcca tgtggaaatg gatactgacc cactgc 36

<210> 38
<211> 627
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(627)

<400> 38

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atg tgg aaa tgg ata ctg acc cac tgc gct tct gct ttc ccg cac ctg   48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
  1               5                  10                  15

ccg ggt tgc tgc tgc tgc tgc ttc ctg ctg ctg ttc ctg gtt tct tct   96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
             20                  25                  30

gtt ccg gtt acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa   144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
         35                  40                  45

gct acc aac tct tcc tct tcc tct ttc tct tcc ccg act tcc gct ggt   192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly
     50                  55                  60

cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt   240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
 65                  70                  75                  80

aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt   288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
                 85                  90                  95

aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag   336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
            100                 105                 110

ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc   384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
        115                 120                 125

aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa   432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
    130                 135                 140
```

```
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga   480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145                 150                 155                 160

tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg   528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
                165                 170                 175

tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca   576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
            180                 185                 190

cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca   624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
        195                 200                 205

tag                                                               627
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<210> 39
<211> 208
<212> PRT
<213> Escherichia coli

<400> 39

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Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
  1               5                  10                  15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
             20                  25                  30
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
         35                  40                  45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly
     50                  55                  60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
 65                  70                  75                  80
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
                85                  90                  95
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
            100                 105                 110
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
        115                 120                 125
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
    130                 135                 140
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145                 150                 155                 160
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
                165                 170                 175
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
            180                 185                 190
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
        195                 200                 205
```

<210> 40
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
tttcatgact tgtcaagctc tgggtcaaga tatggttc 38

<210> 41
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
gcccaagctt ccacaaacgt tgccttcc 28

<210> 42
<211> 525
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(522)

<400> 42

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atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc   48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1               5                  10                  15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac   96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
             20                  25                  30

gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg   144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
         35                  40                  45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt   192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
     50                  55                  60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca   240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65                  70                  75                  80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat   288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                 85                  90                  95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt   336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
            100                 105                 110

aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat   384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
        115                 120                 125

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg   432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
    130                 135                 140
```

```
gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg   480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145                 150                 155                 160

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca tag       525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
                165                 170
```

<210> 43
<211> 174
<212> PRT
<213> Escherichia coli

<400> 43

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Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1               5                  10                  15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
             20                  25                  30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
         35                  40                  45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
     50                  55                  60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65                  70                  75                  80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                 85                  90                  95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
            100                 105                 110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
        115                 120                 125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
    130                 135                 140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145                 150                 155                 160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
                165                 170
```

<210> 44
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 44

```
tcagtgaatt cattaaagag gagaaattaa tcatgacttg ccagg                  45
```

<210> 45
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 45
tcatgacttg ccaggcactg ggtcaagaca tggtttcccc ggaagcta 48

<210> 46
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 46
gcttcagcag cccatctagc gcaggtcgtc acgttcgctc ttacaacc 48

<210> 47
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 47
gttcgttggc gcaaactgtt cagctttacc aagtacttcc tgaaaatc 48

<210> 48
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 48
tcgaaaaaaa cggtaaagtt tctgggac 28

<210> 49
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 49

gatgggctgc tgaagctaga gctggagctg ttggtagctt ccggggaa 48

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 50
aacagtttgc gccaacgaac atcaccctgt aagtggttgt aagag 45

<210> 51
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 51
ttcttggtcc cagaaacttt accgtttttt tcgattttca ggaagta 47

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 52
ttcttggtcc cagaaacttt accg 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 53
agatcaggct tctattatta tgagtgtacc accattggaa gaaag 45

<210> 54
<211> 525
<212> DNA
<213> Escherichia coli

<220>
<221> CDS

<222> (1)..(522)

<400> 54

```
atg act tgc cag gca ctg ggt caa gac atg gtt tcc ccg gaa gct acc   48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1               5                  10                  15

aac agc tcc agc tct agc ttc agc agc cca tct agc gca ggt cgt cac   96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
             20                  25                  30

gtt cgc tct tac aac cac tta cag ggt gat gtt cgt tgg cgc aaa ctg   144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
         35                  40                  45

ttc agc ttt acc aag tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt   192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
     50                  55                  60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca   240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65                  70                  75                  80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat   288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                 85                  90                  95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt   336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
            100                 105                 110

aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat   384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
        115                 120                 125

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg   432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
    130                 135                 140

gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg   480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145                 150                 155                 160

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca tag       525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
                165                 170
```

<210> 55
<211> 174
<212> PRT
<213> Escherichia coli

<400> 55

```
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1               5                  10                  15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
             20                  25                  30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
         35                  40                  45
```

```
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
     50                  55                  60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65                  70                  75                  80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                 85                  90                  95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
            100                 105                 110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
        115                 120                 125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
    130                 135                 140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145                 150                 155                 160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
                165                 170
```

<210> 56
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
ggaccctcat gacctgccag gctctgggtc aggac 35

<210> 57
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
ggacagccat ggctggtcgt cacgttcg 28

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
ggacagccat ggttcgttgg cgtaaactg 29

<210> 59
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
ggacagccat ggaaaaaaac ggtaaagttt c 31

<210> 60
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 60
ggacccccat ggagaactgc ccgtagagc 29

<210> 61
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 61
ggacccccat ggtcaaagcc attaacagca ac 32

<210> 62
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 62
ggacccccat ggggaaactc tatggctcaa aag 33

<210> 63
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 63
ctgcccaagc ttattatgag tgtaccacca ttggaag 37

<210> 64
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 64
ctgcccaagc ttattacttc agcttacagt cattgt 36

<210> 65
<211> 525
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(522)

<400> 65
atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc 48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac 96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg 144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt 192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat 384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg 432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140

gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg 480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca tag 525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser

165 170

<210> 66
<211> 174
<212> PRT
<213> Homo sapiens

<400> 66
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 67
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(444)

<400> 67
atg gct ggt cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt 48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15

cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa 96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30

```
aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc   144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
         35                  40                  45

atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc   192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
     50                  55                  60

att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat   240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
 65                  70                  75                  80

ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag   288
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
                 85                  90                  95

gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat aat ggg   336
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
            100                 105                 110

agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg aga gga   384
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
        115                 120                 125

cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg   432
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
    130                 135                 140

gta cac tca tag                                                  444
Val His Ser
145
```

<210> 68
<211> 147
<212> PRT
<213> Homo sapiens

<400> 68

```
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
  1               5                  10                  15
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
             20                  25                  30
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
         35                  40                  45
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
     50                  55                  60
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
 65                  70                  75                  80
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
                 85                  90                  95
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
            100                 105                 110
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
        115                 120                 125
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
    130                 135                 140
Val His Ser
145
```

<210> 69
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(402)

<400> 69
```
atg gtt cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa   48
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys
  1               5                  10                  15

atc gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg   96
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
             20                  25                  30

tac agc atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc   144
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
         35                  40                  45

aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa   192
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
     50                  55                  60

ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg   240
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
 65                  70                  75                  80

ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat   288
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
                 85                  90                  95

aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg   336
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
            100                 105                 110

aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca   384
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
        115                 120                 125

atg gtg gta cac tca tag                                          402
Met Val Val His Ser
    130
```

<210> 70
<211> 133
<212> PRT
<213> Homo sapiens

<400> 70
```
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys
  1               5                  10                  15
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
             20                  25                  30
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
         35                  40                  45
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
     50                  55                  60
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
```

```
 65                  70                  75                  80
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
                85                  90                  95
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
            100                 105                 110
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
        115                 120                 125
Met Val Val His Ser
    130
```

<210> 71
<211> 354
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(354)

<400> 71

```
atg gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg   48
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
  1               5                  10                  15

tac agc atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc   96
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
             20                  25                  30

aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa   144
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
         35                  40                  45

ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg   192
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
     50                  55                  60

ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat   240
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
 65                  70                  75                  80

aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg   288
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
                85                  90                  95

aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca   336
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
            100                 105                 110

atg gtg gta cac tca tag                                          354
Met Val Val His Ser
        115
```

<210> 72
<211> 117
<212> PRT
<213> Homo sapiens

<400> 72

```
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
```

```
  1               5                  10                  15
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
            20                  25                  30
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
        35                  40                  45
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
    50                  55                  60
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
65                  70                  75                  80
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
                85                  90                  95
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
            100                 105                 110
Met Val Val His Ser
        115
```

<210> 73
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(321)

<400> 73

```
atg gag aac tgc ccg tac agc atc ctg gag ata aca tca gta gaa atc   48
Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile
  1               5                  10                  15

gga gtt gtt gcc gtc aaa gcc att aac agc aac tat tac tta gcc atg   96
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met
            20                  25                  30

aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt   144
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
        35                  40                  45

aag ctg aag gag agg ata gag gaa aat gga tac aat acc tat gca tca   192
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser
    50                  55                  60

ttt aac tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga   240
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly
65                  70                  75                  80

aaa gga gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct   288
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser
                85                  90                  95

gct cac ttt ctt cca atg gtg gta cac tca tag                      321
Ala His Phe Leu Pro Met Val Val His Ser
            100                 105
```

<210> 74
<211> 106
<212> PRT
<213> Homo sapiens

<400> 74
Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile
1 5 10 15
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met
20 25 30
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
35 40 45
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser
50 55 60
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly
65 70 75 80
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser
85 90 95
Ala His Phe Leu Pro Met Val Val His Ser
100 105

<210> 75
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(261)

<400> 75
atg gtc aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag 48
Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys
1 5 10 15

ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag 96
Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
20 25 30

gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg 144
Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp
35 40 45

cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct 192
Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala
50 55 60

cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt 240
Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe
65 70 75 80

ctt cca atg gtg gta cac tca tag 264
Leu Pro Met Val Val His Ser
85

<210> 76
<211> 87
<212> PRT
<213> Homo sapiens

<400> 76
Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys
1 5 10 15

```
Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
            20                  25                  30

Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp
        35                  40                  45

Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala
    50                  55                  60

Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe
65                  70                  75                  80

Leu Pro Met Val Val His Ser
                85
```

<210> 77
<211> 219
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(219)

<400> 77

```
atg ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg   48
Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
  1               5                  10                  15

aag gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac   96
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
            20                  25                  30

tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga   144
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
        35                  40                  45

gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac   192
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
    50                  55                  60

ttt ctt cca atg gtg gta cac tca tag                              219
Phe Leu Pro Met Val Val His Ser
65                  70
```

<210> 78
<211> 72
<212> PRT
<213> Homo sapiens

<400> 78

```
Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
  1               5                  10                  15
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
            20                  25                  30
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
        35                  40                  45
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
    50                  55                  60
```

```
Phe Leu Pro Met Val Val His Ser
 65                  70
```

<210> 79
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(357)

<400> 79

```
atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc   48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1               5                  10                  15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac   96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
             20                  25                  30

gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg   144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
         35                  40                  45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt   192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
     50                  55                  60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca   240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65                  70                  75                  80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat   288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                 85                  90                  95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt   336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
            100                 105                 110

aac aat gac tgt aag ctg aag                                      357
Asn Asn Asp Cys Lys Leu Lys
        115
```

<210> 80
<211> 119
<212> PRT
<213> Homo sapiens

<400> 80

```
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
  1               5                  10                  15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
             20                  25                  30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
         35                  40                  45
```

```
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
     50                  55                  60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65                  70                  75                  80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
                 85                  90                  95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
            100                 105                 110

Asn Asn Asp Cys Lys Leu Lys
        115
```

<210> 81
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(276)

<400> 81

```
atg gct ggt cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt   48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
  1               5                  10                  15

cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa   96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
            20                  25                  30

aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc   144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
        35                  40                  45

atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc   192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
    50                  55                  60

att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat   240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65                  70                  75                  80

ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag                   276
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
                85                  90
```

<210> 82
<211> 92
<212> PRT
<213> Homo sapiens

<400> 82

```
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
  1               5                  10                  15

Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
```

20 25 30

Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45

Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60

Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
85 90

<210> 83
<211> 525
<212> DNA
<213> Homo sapiens

<400> 83
atgacctctc aggctctggg tcaggacatg gtttctccgg aagctaccaa ctcttcctct 60
tcctctttct cttccccgtc ttccgctggt cgtcacgttc gttcttacaa ccacctgcag 120
ggtgacgttc gttggcgtaa actgttctct ttcaccaaat acttcctgaa aatcgaaaaa 180
aacggtaaag tttctgggac caagaaggag aactctccgt acagcatcct ggagataaca 240
tcagtagaaa tcggagttgt tgccgtcaaa gccattaaca gcaactatta cttagccatg 300
aacaagaagg ggaaactcta tggctcaaaa gaatttaaca atgactgtaa gctgaaggag 360
aggatagagg aaaatggata caatacctat gcatcattta actggcagca taatgggagg 420
caaatgtatg tggcattgaa tggaaaagga gctccaagga gaggacagaa aacacgaagg 480
aaaaacacct ctgctcactt tcttccaatg gtggtacact catag 525

<210> 84
<211> 525
<212> DNA
<213> Homo sapiens

<400> 84
atgacctgcc aggctctggg tcaggacatg gtttctccgg aagctaccaa ctcttcctct 60
tcctctttct cttccccgtc ttccgctggt cgtcacgttc gttcttacaa ccacctgcag 120
ggtgacgttc gttggcgtaa actgttctct ttcaccaaat acttcctgaa aatcgaaaaa 180
aacggtaaag tttctgggac caagaaggag aactctccgt acagcatcct ggagataaca 240
tcagtagaaa tcggagttgt tgccgtcaaa gccattaaca gcaactatta cttagccatg 300
aacaagaagg ggaaactcta tggctcaaaa gaatttaaca atgactgtaa gctgaaggag 360
aggatagagg aaaatggata caatacctat gcatcattta actggcagca taatgggagg 420
caaatgtatg tggcattgaa tggaaaagga gctccaagga gaggacagaa aacacgaagg 480
aaaaacacct ctgctcactt tcttccaatg gtggtacact catag 525

<210> 85
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 85
ggaccctcat gacctctcag gctctgggt 29

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 86
aaggagaact ctccgtacag c 21

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 87
gctgtacggt ctgttctcct t 21

<210> 88
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
ggaccctcat gacctgccag gctctgggtc aggac 35

<210> 89
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctgcccaagc ttattatgag tgtaccacca ttggaag 37

<210> 90
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 90
aaaggatcct gccaggctct gggtcaggac atg 33

<210> 91
<211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 92
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
gggcccaagc ttatgagtgt accaccat 28

<210> 93
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 93
ccggcggatc ccatatgtct tacaaccacc tgcagg 36

<210> 94
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
ccggcggtac cttattatga gtgtaccacc attgg 35

<210> 95
<211> 426
<212> DNA
<213> Homo sapiens

<400> 95
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcataa 426

<210> 96
<211> 141
<212> PRT
<213> Homo sapiens

<400> 96
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 97
caaccacctg cagggtgacg 20

<210> 98
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 98
aacggtcgac aaatgtatgt ggcactgaac ggtaaaggtg ctccacgtcg tggtcagaaa 60
acccgtcgta aaaacacc 78

<210> 99

<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 99
gggcccaagc ttaagagtgt accaccattg gcagaaagtg agcagaggtg tttttacgac 60
gggttttctg accacg 76

<210> 100
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 100
gccacataca tttgtcgacc gtt 23

<210> 101
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 101
gggcccaagc ttaagagtg 19

<210> 102
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 102
gccacataca tttgtcgacc gtt 23

<210> 103
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 103

ctgcagggtg acgttcgttg gcgtaaactg ttctccttca ccaaatactt cctgaaaatc 60
gaaaaaaacg gtaaagtttc tggtaccaag 90

<210> 104
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 104
agctttaaca gcaacaacac cgatttcaac ggaggtgatt tccaggatgg agtacgggca 60
gttttctttc ttggtaccag aaactttacc 90

<210> 105
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 105
ggtgttgttg ctgttaaagc tatcaactcc aactactacc tggctatgaa caagaaaggt 60
aaactgtacg gttccaaaga atttaacaac 90

<210> 106
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 106
gtcgaccgtt gtgctgccag ttgaaggaag cgtaggtgtt gtaaccgttt tcttcgatac 60
gttctttcag tttacagtcg ttgttaaatt ctttggaacc 100

<210> 107
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 107
gcggcgtcga ccgttgtgct gccag 25

<210> 108
<211> 26
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 108
gcggcctgca gggtgacgtt cgttgg 26

<210> 109
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 109
ccggcggatc ccatatgtct tacaaccacc tgcagg 36

<210> 110
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 110
cgcgcgatat cttattaaga gtgtaccacc attg 34

<210> 111
<211> 426
<212> DNA
<213> Homo sapiens

<400> 111
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc cttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggta ccaagaaaga aaactgcccg 120
tactccatcc tggaaatcac ctccgttgaa atcggtgttg ttgctgttaa agctatcaac 180
tccaactact acctggctat gaacaagaaa ggtaaactgt acggttccaa agaatttaac 240
aacgactgta aactgaaaga acgtatcgaa gaaaacggtt acaacaccta cgcttccttc 300
aactggcagc acaacggtcg acaaatgtat gtggcactga acggtaaagg tgctccacgt 360
cgtggtcaga aaacccgtcg taaaaacacc tctgctcact ttctgccaat ggtggtacac 420
tcttaa 426

<210> 112
<211> 141
<212> PRT
<213> Homo sapiens

<400> 112
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser

20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 113
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 113
cgcggccatg gctctgggtc aggacatg 28

<210> 114
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 114
gggcccaagc ttatgagtgt accaccat 28

<210> 115
<211> 516
<212> DNA
<213> Homo sapiens

<400> 115
atggctctgg gtcaagatat ggtttctccg gaagctacca actcttcctc ttcctctttc 60
tcttccccgt cttccgctgg tcgtcacgtt cgttcttaca accacctgca gggtgacgtt 120
cgttggcgta aactgttctc tttcaccaaa tacttcctga aaatcgaaaa aaacggtaaa 180
gtttctggga ccaagaagga gaactgcccg tacagcatcc tggagataac atcagtagaa 240
atcggagttg ttgccgtcaa agccattaac agcaactatt acttagccat gaacaagaag 300
gggaaactct atggctcaaa agaatttaac aatgactgta agctgaagga gaggatagag 360

gaaaatggat acaataccta tgcatcattt aactggcagc ataatgggag gcaaatgtat 420
gtggcattga atggaaaagg agctccaagg agaggacaga aaacacgaag gaaaaacacc 480
tctgctcact ttcttccaat ggtggtacac tcataa 516

<210> 116
<211> 171
<212> PRT
<213> Homo sapiens

<400> 116
Met Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser
1 5 10 15

Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser
20 25 30

Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe
35 40 45

Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr
50 55 60

Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu
65 70 75 80

Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala
85 90 95

Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp
100 105 110

Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala
115 120 125

Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn
130 135 140

Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr
145 150 155 160

Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 117
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 117
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 118
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 118
ctgcccaagc ttttatgagt gtaccaccat tggaagaaag tgagcagagg tgtttttttc 60
tcgtgttttc tgtcc 75

<210> 119
<211> 426
<212> DNA
<213> Homo sapiens

<400> 119
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaga aaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 120
<211> 141
<212> PRT
<213> Homo sapiens

<400> 120
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Glu Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 121
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 121
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 122
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 122
ctgcccaagc ttttatgagt gtaccaccat tggaagaaag tgagcagagg tgtttttctg 60
tcgtgttttc tgtcc 75

<210> 123
<211> 426
<212> DNA
<213> Homo sapiens

<400> 123
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaca gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 124
<211> 141
<212> PRT
<213> Homo sapiens

<400> 124
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Gln Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 125
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 125
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 126
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 126
ctgcccaagc ttttatgagt gtaccaccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgtttcc tgtcctctcc ttgg 84

<210> 127
<211> 426
<212> DNA
<213> Homo sapiens

<400> 127
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacagg aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 128
<211> 141
<212> PRT
<213> Homo sapiens

<400> 128
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Glu Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 129
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 129
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 130
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 130
ctgcccaagc ttttatgagt gtaccaccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgtctgc tgtcctctcc ttgg 84

<210> 131
<211> 426
<212> DNA
<213> Homo sapiens

<400> 131
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacagc agacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 132
<211> 141

<212> PRT
<213> Homo sapiens

<400> 132
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Gln Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 133
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 133
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 134
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 134
ctgcccaagc ttttatgagt gtaccaccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgttttc tgtccttccc ttggagctcc ttt 93

<210> 135
<211> 426
<212> DNA
<213> Homo sapiens

<400> 135
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
gaaggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 136
<211> 140
<212> PRT
<213> Homo sapiens

<400> 136
Met Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser
1 5 10 15

Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly
20 25 30

Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val
35 40 45

Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu
50 55 60

Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn
65 70 75 80

Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
85 90 95

Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu
100 105 110

Asn Gly Lys Gly Ala Pro Arg Glu Gly Gln Lys Thr Arg Arg Lys Asn
115 120 125

Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 137
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 137
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 138
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 138
ctgcccaagc ttttatgagt gtaccaccat tggaagaaag tgagcagagg tgtttttcct 60
tcgtgttttc tgtccctgcc ttggagctcc ttt 93

<210> 139
<211> 426
<212> DNA
<213> Homo sapiens

<400> 139
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
cagggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 140
<211> 141
<212> PRT
<213> Homo sapiens

<400> 140
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Gln Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 141
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 141
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 142
ttgaatggag aaggagctcc a 21

<210> 143
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 143
tggagctcct tctccattca a 21

<210> 144
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 144
ctgcccaagc ttttatgagt gtaccaccat tgg 33

<210> 145
<211> 426
<212> DNA
<213> Homo sapiens

<400> 145
atgtcttaca accacctgca gggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcatcattt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggagaagg agctccaagg 360
agaggacaga aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 146
<211> 141
<212> PRT

<213> Homo sapiens

<400> 146
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Glu Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 147
<211> 3974
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHE4-5 vector

<400> 147
ggtacctaag tgagtagggc gtccgatcga cggacgcctt ttttttgaat tcgtaatcat 60
ggtcatagct gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag 120
ccggaagcat aaagtgtaaa gcctggggtg cctaatgagt gagctaactc acattaattg 180
cgttgcgctc actgcccgct ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa 240
tcggccaacg cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca 300
ctgactcgct gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg 360
taatacggtt atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc 420
agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc 480
cccctgacga gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac 540
tataaagata ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc 600
tgccgcttac cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata 660
gctcacgctg taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc 720
acgaaccccc cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca 780
acccggtaag acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag 840
cgaggtatgt aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta 900
gaagaacagt atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg 960
gtagctcttg atccggcaaa caaaccaccg ctggtagcgg tggttttttt gtttgcaagc 1020
agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt 1080
ctgacgctca gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcgtcga 1140
caattcgcgc gcgaaggcga agcggcatgc atttacgttg acaccatcga atggtgcaaa 1200
acctttcgcg gtatggcatg atagcgcccg gaagagagtc aattcagggt ggtgaatgtg 1260
aaaccagtaa cgttatacga tgtcgcagag tatgccggtg tctcttatca gaccgtttcc 1320

cgcgtggtga accaggccag ccacgtttct gcgaaaacgc gggaaaaagt ggaagcggcg 1380
atggcggagc tgaattacat tcccaaccgc gtggcacaac aactggcggg caaacagtcg 1440
ttgctgattg gcgttgccac ctccagtctg gccctgcacg cgccgtcgca aattgtcgcg 1500
gcgattaaat ctcgcgccga tcaactgggt gccagcgtgg tggtgtcgat ggtagaacga 1560
agcggcgtcg aagcctgtaa agcggcggtg cacaatcttc tcgcgcaacg cgtcagtggg 1620
ctgatcatta actatccgct ggatgaccag gatgccattg ctgtggaagc tgcctgcact 1680
aatgttccgg cgttatttct tgatgtctct gaccagacac ccatcaacag tattattttc 1740
tcccatgaag acggtacgcg actgggcgtg gagcatctgg tcgcattggg tcaccagcaa 1800
atcgcgctgt tagcgggccc attaagttct gtctcggcgc gtctgcgtct ggctggctgg 1860
cataaatatc tcactcgcaa tcaaattcag ccgatagcgg aacgggaagg cgactggagt 1920
gccatgtccg gttttcaaca aaccatgcaa atgctgaatg agggcatcgt tcccactgcg 1980
atgctggttg ccaacgatca gatggcgctg ggcgcaatgc gcgccattac cgagtccggg 2040
ctgcgcgttg gtgcggatat ctcggtagtg ggatacgacg ataccgaaga cagctcatgt 2100
tatatcccgc cgttaaccac catcaaacag gattttcgcc tgctggggca aaccagcgtg 2160
gaccgcttgc tgcaactctc tcagggccag gcggtgaagg gcaatcagct gttgcccgtc 2220
tcactggtga aaagaaaaac caccctggcg cccaatacgc aaaccgcctc tccccgcgcg 2280
ttggccgatt cattaatgca gctggcacga caggtttccc gactggaaag cgggcagtga 2340
gcgcaacgca attaatgtaa gttagcgcga attgtcgacc aaagcggcca tcgtgcctcc 2400
ccactcctgc agttcggggg catggatgcg cggatagccg ctgctggttt cctggatgcc 2460
gacggatttg cactgccggt agaactccgc gaggtcgtcc agcctcaggc agcagctgaa 2520
ccaactcgcg aggggatcga gcccggggtg ggcgaagaac tccagcatga gatccccgcg 2580
ctggaggatc atccagccgg cgtcccggaa aacgattccg aagcccaacc tttcatagaa 2640
ggcggcggtg gaatcgaaat ctcgtgatgg caggttgggc gtcgcttggt cggtcatttc 2700
gaaccccaga gtcccgctca gaagaactcg tcaagaaggc gatagaaggc gatgcgctgc 2760
gaatcgggag cggcgatacc gtaaagcacg aggaagcggt cagcccattc gccgccaagc 2820
tcttcagcaa tatcacgggt agccaacgct atgtcctgat agcggtccgc cacacccagc 2880
cggccacagt cgatgaatcc agaaaagcgg ccattttcca ccatgatatt cggcaagcag 2940
gcatcgccat gggtcacgac gagatcctcg ccgtcgggca tgcgcgcctt gagcctggcg 3000
aacagttcgg ctggcgcgag cccctgatgc tcttcgtcca gatcatcctg atcgacaaga 3060
ccggcttcca tccgagtacg tgctcgctcg atgcgatgtt tcgcttggtg gtcgaatggg 3120
caggtagccg gatcaagcgt atgcagccgc cgcattgcat cagccatgat ggatactttc 3180
tcggcaggag caaggtgaga tgacaggaga tcctgccccg gcacttcgcc caatagcagc 3240
cagtcccttc ccgcttcagt gacaacgtcg agcacagctg cgcaaggaac gcccgtcgtg 3300
gccagccacg atagccgcgc tgcctcgtcc tgcagttcat tcagggcacc ggacaggtcg 3360
gtcttgacaa aaagaaccgg gcgcccctgc gctgacagcc ggaacacggc ggcatcagag 3420
cagccgattg tctgttgtgc ccagtcatag ccgaatagcc tctccaccca agcggccgga 3480
gaacctgcgt gcaatccatc ttgttcaatc atgcgaaacg atcctcatcc tgtctcttga 3540
tcagatcttg atcccctgcg ccatcagatc cttggcggca agaaagccat ccagtttact 3600
ttgcagggct tcccaacctt accagagggc gccccagctg gcaattccgg ttcgcttgct 3660
gtccataaaa ccgcccagtc tagctatcgc catgtaagcc cactgcaagc tacctgcttt 3720
ctctttgcgc ttgcgttttc ccttgtccag atagcccagt agctgacatt catccggggt 3780
cagcaccgtt tctgcggact ggctttctac gtgttccgct tcctttagca gcccttgcgc 3840
cctgagtgct tgcggcagcg tgaagcttaa aaaactgcaa aaaatagttt gacttgtgag 3900
cggataacaa ttaagatgta cccaattgtg agcggataac aatttcacac attaaagagg 3960
agaaattaca tatg 3974

<210> 148
<211> 112
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHE4-5
promoter sequence

<400> 148
aagcttaaaa aactgcaaaa aatagtttga cttgtgagcg gataacaatt aagatgtacc 60
caattgtgag cggataacaa tttcacacat taaagaggag aaattacata tg 112

<210> 149

<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 149
gagcgcggat ccgccaccat gaaggtctcc gtggctgccc tctcctgcct catgcttgtt 60
actgcccttg gatctcaggc cagctacaat caccttcaag gagatg 106

<210> 150
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 150
gagcgcggat ccctatgagt gtaccaccat tggaag 36

<210> 151
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 151
ccggccatat gcgtaaactg ttctctttca cc 32

<210> 152
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 152
ccggcggtac cttattatga gtgtaccacc attgg 35

<210> 153
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 153
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 154
<211> 39

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 154
gatcgcggta ccttattatg agtgtaccac cattggaag 39

<210> 155
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 155
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 156
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 156
gatcgcggta ccttattatg agtgtaccac cattggaag 39

<210> 157
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 157
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 158
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 158
gatcgcggta ccttattatg agtgtaccac cattggaag 39

<210> 159
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 160
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gatcgcggta ccttattatg agtgtaccac cattggaag 39

<210> 161
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gatcgcggat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 162
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 163
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gatcgcggat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 164
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 165
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gatcgcggat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 166
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 167
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gatcgcggat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 168
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 169
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 170
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gatcgcggta ccttattatg agtgtaccac cattggaag 39

<210> 171
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 171
gatcgccata tggctggtcg tcacgttcgt tc. 32

<210> 172
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 172
gatcgcggta ccttattatg agtgtaccac cattggaag 39

<210> 173
<211> 456
<212> DNA
<213> Escherichia coli

<400> 173
catatggctg gtcgtcacgt tcgttcttac aaccacctgc agggtgacgt tcgttggcgt 60
aaactgttct ctttcaccaa atacttcctg aaaatcgaaa aaaacggtaa agtttctggg 120
accaagaagg agaactgccc gtacagcatc ctggagataa catcagtaga aatcggagtt 180
gttgccgtca aagccattaa cagcaactat tacttagcca tgaacaagaa ggggaaactc 240
tatggctcaa aagaatttaa caatgactgt aagctgaagg agaggataga ggaaaatgga 300
tacaatacct atgcatcatt taactggcag cataatggga ggcaaatgta tgtggcattg 360
aatggaaaag gagctccaag gagaggacag aaaacacgaa ggaaaaacac ctctgctcac 420
tttcttccaa tggtggtaca ctcataataa ggtacc 456

<210> 174
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 174

gactacatat ggctggtcgt cacgttcgtt cttacaacca cctgcagg 48

<210> 175
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 175
ctagtctcta gattattatg agtgtacaac catcggcagg aagtgag 47

<210> 176
<211> 447
<212> DNA
<213> Escherichia coli

<400> 176
atggctggtc gtcacgttcg ttcttacaac cacctgcagg gtgacgttcg ttggcgtaaa 60
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aagaaagaaa actgcccgta ctctatcctg gaaatcacct ccgttgaaat cggtgttgta 180
gccgttaaag ccatcaactc caactattac ctggccatga acaaaaaggg taaactgtac 240
ggctctaaag aattcaacaa cgactgcaaa ctgaaagaac gtatcgaaga gaacggttac 300
aacacctacg catccttcaa ctggcagcac aacggtcgtc agatgtacgt tgcactgaac 360
ggtaaaggcg ctccgcgtcg cggtcagaaa acccgtcgca aaaacacctc tgctcacttc 420
ctgccgatgg ttgtacactc ataataa 447

Applicant's or agent's file reference number 1488.036PC0K	International application No. PCT/US00/18328

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13*bis*)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 412, line 29.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution
American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
03 July 2000	PTA-2183

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

(DNA Plasmid (Human): pHE4.KGF-2.A63-S208)

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Applicant's or agent's file reference number 1488.036PC0K	International application No. PCT/US00/18328

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AUSTRALIA

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CANADA

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DENMARK

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FINLAND

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NETHERLANDS

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Applicant's or agent's file reference number 1488.036PC0K	International application No. PCT/US00/18328

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AUSTRALIA

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FINLAND

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ICELAND

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UNITED KINGDOM

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Applicant's or agent's file reference number 1488.036PC0K	International application No. (TO BE ASSIGNED)

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(PCT Rule 13*bis*)

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10801 University Boulevard
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Date of deposit	Accession Number
03 July 2000	TO BE ADVISED

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

(TO BE ADVISED)

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AUSTRALIA

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(DNA Plasmid (TO BE ADVISED))

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Applicant's or agent's file reference number 1488.036PC0K	International application No. (TO BE ASSIGNED)

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Applicant's or agent's file reference number 1488.036PC0K	International application No. (TO BE ASSIGNED)

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10801 University Boulevard
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Date of deposit	Accession Number
January 9, 1998	209575

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA Plasmid pHEKGF-2delta33

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Authorized officer	Authorized officer

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

CANADA

The applicant hereby requests that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent office or any person approved by the applicant in the individual case.

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the National Board of Patents and Registration or any person approved by the applicant in the individual case.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

NORWAY

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SINGAPORE

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SWEDEN

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UNITED KINGDOM

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Applicant's or agent's file reference number 1488.036PC0K	International application No. (TO BE ASSIGNED)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13*bis*)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 399, line 19.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution
American Type Culture Collection

Address of depositary institution *(including postal code and country)*

10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
June 30, 1999	PTA-289

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA Plasmid pVGI-0:Δ33 KGF2 (Ref. PF155)

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the international Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

AUSTRALIA

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CANADA

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DENMARK

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FINLAND

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ICELAND

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NETHERLANDS

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NORWAY

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SWEDEN

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UNITED KINGDOM

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Applicant's or agent's file reference number 1488.036PC0K	International application No. (TO BE ASSIGNED)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13*bis*)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 399, line 11.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution
American Type Culture Collection

Address of depositary institution *(including postal code and country)*

10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
June 30, 1999	PTA-290

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA Plasmid pVGI-0: KGF2 (F.L.) (Ref. PF155)

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the international Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

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☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

CANADA

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DENMARK

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FINLAND

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ICELAND

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NETHERLANDS

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NORWAY

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SWEDEN

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UNITED KINGDOM

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Applicant's or agent's file reference number 1488.036PC0K	International application No. (TO BE ASSIGNED)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13*bis*)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 20, line 21.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution
American Type Culture Collection

Address of depositary institution *(including postal code and country)*

10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
September 29, 1994	75901

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA Plasmid, 366,885

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(If the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the international Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☐ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

AUSTRALIA

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CANADA

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DENMARK

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FINLAND

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ICELAND

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

NORWAY

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SINGAPORE

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SWEDEN

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UNITED KINGDOM

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Applicant's or agent's file reference number	1488.036PC0K	International application No. (TO BE ASSIGNED)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13*bis*)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 4, line 11.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution
American Type Culture Collection

Address of depositary institution *(including postal code and country)*

10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
December 16, 1994	75977

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

DNA Plasmid, 366885A

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Authorized officer	Authorized officer

AUSTRALIA

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CANADA

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DENMARK

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FINLAND

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NETHERLANDS

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UNITED KINGDOM

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/18328

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :Please See Extra Sheet.
US CL :Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350, 399; 536/23.1, 23.5; 435/69.4, 71.1, 71.2, 325, 471, 252.3, 254.11, 320.1; 514/2, 8, 12, 866, 885, 893

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim
A	WO 98/16642 A1 (AMGEN INC.) 23 April 1998 (23/04/98), see entire document.	1-12
A	WO 98/16243 A1 (AMGEN INC.) 23 April 1998 (23/04/98), see entire document.	1-12

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or prior date and not in conflict with the application but cited to understa the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot considered novel or cannot be considered to involve an inventive s when the document is taken alone
"B"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot considered to involve an inventive step when the document combined with one or more other such documents, such combinat being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 06 SEPTEMBER 2000	Date of mailing of the international search report 10 OCT 2000
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer PREMA MERTZ Telephone No. (703) 308-0196

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/18328

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (7):

C07K 14/47, 14/475; C12N 5/10, 15/12, 15/16, 15/63, 15/64; A61K 38/16, 38/17, 38/18

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

530/350, 399; 536/23.1, 23.5; 435/69.4, 71.1, 71.2, 325, 471, 252.3, 254.11, 320.1; 514/2, 8, 12, 866, 885, 893

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

WEST, CAS ONLINE, MEDLINE, CAPLUS
search terms: keratinocyte growth factor-2, fibroblast growth factor-12, mutein, mutant, recombinant, method, administer, therapy, treatment.